SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Ruben, Steven M

  (ii) TITLE OF INVENTION: Apoptosis Inducing Molecule I

 (iii) NUMBER OF SEQUENCES: 10

  (iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: Human Genome Sciences, Inc.
     (B) STREET: 9410 Key West Avenue
     (C) CITY: Rockville
     (D) STATE: MD
     (E) COUNTRY: US
     (F) ZIP: 20850

   (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

  (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER:
     (B) FILING DATE: 13-MAR-1997
     (C) CLASSIFICATION:

 (viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME: Kimball, Paul, C.
     (B) REGISTRATION NUMBER: 34,610
     (C) REFERENCE/DOCKET NUMBER: PF261

  (ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: (301) 309-8504
     (B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 1643 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

  (ii) MOLECULE TYPE: DNA (genomic)

  (ix) FEATURE:
     (A) NAME/KEY: CDS
     (B) LOCATION: 52..894

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGCACGAGCG GCTGCCTGGC TGACTTACAG CAGTCAGACT CTGACAGGTT C ATG GCT        57
                                                         Met Ala
                                                           1
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```
ATG ATG GAG GTC CAG GGG GGA CCC AGC CTG GGA CAG ACC TGC GTG CTG          105
Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys Val Leu
         5                   10                  15

ATC GTG ATC TTC ACA GTG CTC CTG CAG TCT CTC TGT GTG GCT GTA ACT          153
Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala Val Thr
        20                   25                  30

TAC GTG TAC TTT ACC AAC GAG CTG AAG CAG ATG CAG GAC AAG TAC TCC          201
Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys Tyr Ser
        35                   40                  45                  50

AAA AGT GGC ATT GCT TGT TTC TTA AAA GAA GAT GAC AGT TAT TGG GAC          249
Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr Trp Asp
                    55                   60                  65

CCC AAT GAC GAA GAG AGT ATG AAC AGC CCC TGC TGG CAA GTC AAG TGG          297
Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val Lys Trp
                70                   75                  80

CAA CTC CGT CAG CTC GTT AGA AAG ATG ATT TTG AGA ACC TCT GAG GAA          345
Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser Glu Glu
        85                   90                  95

ACC ATT TCT ACA GTT CAA GAA AAG CAA CAA AAT ATT TCT CCC CTA GTG          393
Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro Leu Val
        100                  105                 110

AGA GAA AGA GGT CCT CAG AGA GTA GCA GCT CAC ATA ACT GGG ACC AGA          441
Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly Thr Arg
115                  120                  125                 130

GGA AGA AGC AAC ACA TTG TCT TCT CCA AAC TCC AAG AAT GAA AAG GCT          489
Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala
                    135                  140                 145

CTG GGC CGC AAA ATA AAC TCC TGG GAA TCA TCA AGG AGT GGG CAT TCA          537
Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly His Ser
                    150                  155                 160

TTC CTG AGC AAC TTG CAC TTG AGG AAT GGT GAA CTG GTC ATC CAT GAA          585
Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile His Glu
                165                  170                 175

AAA GGG TTT TAC TAC ATC TAT TCC CAA ACA TAC TTT CGA TTT CAG GAG          633
Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu
        180                  185                 190

GAA ATA AAA GAA AAC ACA AAG AAC GAC AAA CAA ATG GTC CAA TAT ATT          681
Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln Tyr Ile
195                      200                  205                 210

TAC AAA TAC ACA AGT TAT CCT GAC CCT ATA TTG TTG ATG AAA AGT GCT          729
Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys Ser Ala
                    215                  220                 225

AGA AAT AGT TGT TGG TCT AAA GAT GCA GAA TAT GGA CTC TAT TCC ATC          777
Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile
                    230                  235                 240
```

2

```
TAT CAA GGG GGA ATA TTT GAG CTT AAG GAA AAT GAC AGA ATT TTT GTT      825
Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile Phe Val
        245              250              255

TCT GTA ACA AAT GAG CAC TTG ATA GAC ATG GAC CAT GAA GCC AGT TTT      873
Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala Ser Phe
        260              265              270

TTC GGG GCC TTT TTA GTT GGC TAACTGACCT GGAAAGAAAA AGCAATAACC         924
Phe Gly Ala Phe Leu Val Gly
275              280

TCAAAGTGAC TATTCAGTTT TCAGGATGAT ACACTATGAA GATGTTTCAA AAAATCTGAC    984

CAAAACAAAC AAACAGAAAA CAGAAAACAA AAAAACCTCT ATGCAATCTG AGTAGAGCAG   1044

CCACAACCAA AAAATTCTAC AACACACACT GTTCTGAAAG TGACTCACTT ATCCCAAGAA   1104

AATGAAATTG CTGAAAGATC TTTCAGGACT CTACCTCATA TCAGTTTGCT AGCAGAAATC   1164

TAGAAGACTG TCAGCTTCCA AACATTAATG CAATGGTTAA CATCTTCTGT CTTTATAATC   1224

TACTCCTTGT AAAGACTGTA GAAGAAAGCG CAACAATCCA TCTCTCAAGT AGTGTATCAC   1284

AGTAGTAGCC TCCAGGTTTC CTTAAGGGAC AACATCCTTA AGTCAAAAGA GAGAAGAGGC   1344

ACCACTAAAA GATCGCAGTT TGCCTGGTGC AGTGGCTCAC ACCTGTAATC CCAACATTTT   1404

GGGAACCCAA GGTGGGTAGA TCACGAGATC AAGAGATCAA GACCATAGTG ACCAACATAG   1464

TGAAACCCCA TCTCTACTGA AAGTGCAAAA ATTAGCTGGG TGTGTTGGCA CATGCCTGTA   1524

GTCCCAGCTA CTTGAGAGGC TGAGGCAGGA GAATCGTTTG AACCCGGGAG GCAGAGGTTG   1584

CAGTGTGGTG AGATCATGCC ACTACACTCC AGCCTGGCGA CAGAGCGAGA CTTGGTTTC   1643
```

(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 281 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
 1               5                  10                  15

Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
            20                  25                  30

Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
        35                  40                  45

Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
     50                  55                  60
```

```
Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val
65              70              75              80

Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
            85              90              95

Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
        100             105             110

Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
        115             120             125

Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
        130             135             140

Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
145             150             155             160

His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
        165             170             175

His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
        180             185             190

Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
        195             200             205

Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
    210             215             220

Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
225             230             235             240

Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
            245             250             255

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
        260             265             270

Ser Phe Phe Gly Ala Phe Leu Val Gly
    275             280
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 267 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Val Asp Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu
1               5               10              15
```

```
Pro Cys Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro
            20              25              30

Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro
        35              40              45

Leu Pro Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser
    50              55              60

Thr Gly Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu
65              70              75                      80

Val Gly Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu
            85              90                      95

Leu Ala Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser
            100             105             110

Leu Glu Lys Gln Ile Gly His Pro Ser Pro Pro Pro Glu Lys Lys Glu
        115             120             125

Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met
    130             135             140

Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val
145             150             155                     160

Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe
            165             170             175

Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro
            180             185             190

Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu
        195             200             205

Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met
    210             215             220

Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala
225             230             235             240

Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu
            245             250             255

Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
            260             265
```

(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 279 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Gln Gln Pro Met Asn Tyr Pro Cys Pro Gln Ile Phe Trp Val Asp
1                5                10                15

Ser Ser Ala Thr Ser Ser Trp Ala Pro Pro Gly Ser Val Phe Pro Cys
            20              25                  30

Pro Ser Cys Gly Pro Arg Gly Pro Asp Gln Arg Arg Pro Pro Pro Pro
        35              40              45

Pro Pro Pro Val Ser Pro Leu Pro Pro Pro Ser Gln Pro Leu Pro Leu
    50              55                  60

Pro Pro Leu Thr Pro Leu Lys Lys Lys Asp His Asn Thr Asn Leu Trp
65              70              75                          80

Leu Pro Val Val Phe Phe Met Val Leu Val Ala Leu Val Gly Met Gly
            85              90                  95

Leu Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu
            100             105             110

Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys Gln
        115             120             125

Ile Ala Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser Val
    130             135             140

Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp
145             150             155                         160

Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys
            165             170             175

Gly Gly Leu Val Ile His Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys
            180             185             190

Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His Lys
        195             200             205

Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met Glu
    210             215             220

Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser
225             230             235                         240

Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr
            245             250             255

Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr
            260             265             270

Phe Phe Gly Leu Tyr Lys Leu
            275
```

(2) INFORMATION FOR SEQ ID NO:5:

```
Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
1               5               10              15

Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
            20              25              30

Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
            35              40              45

Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Ser Pro
    50              55              60

Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
65              70              75              80

Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
            85              90              95

Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
            100             105             110

Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
            115             120             125

Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
    130             135             140

Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
145             150             155             160

Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
            165             170             175

Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
            180             185             190

Pro Ile Tyr Leu Gly Cys Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
            195             200             205

Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
    210             215             220

Gln Val Tyr Phe Gly Ile Ile Ala Leu
225             230
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 205 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

    Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
    1   5   10   15

    Leu His Leu Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
                    20   25   30

    Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala
                35   40   45

    Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
        50   55   60

    Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
    65   70   75   80

    Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
                    85   90   95

    Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
                100   105   110

    Val Val Phe Ser Cys Lys Ala Tyr Ser Pro Lys Ala Pro Ser Ser Pro
            115   120   125

    Leu Tyr Leu Ala His Glu Val Cys Leu Phe Ser Ser Gln Tyr Pro Phe
        130   135   140

    His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
    145   150   155   160

    Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
                165   170   175

    Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
                180   185   190

    Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
        195   200   205

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCGGCGGGAT CCATGGCTAT GATGGAGGTC CAG   33

(2) INFORMATION FOR SEQ ID NO:8:

          (i) SEQUENCE CHARACTERISTICS:
           . (A) LENGTH: 33 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGCGCGTCTA GAGCTTAGGC AACTAAAAAG GCC   33

(2) INFORMATION FOR SEQ ID NO:9:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 34 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGCGCGGAT CCATCATGGC TATGATGGAG GTCC   34

(2) INFORMATION FOR SEQ ID NO:10:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 33 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGCGTCTA GAGCTTAGCC AACTAAAAAG GCC   33